

Jason

List of Publications by Year in descending order

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37
papers

1,933
citations

471477

17
h-index

330122

37
g-index

37
all docs

37
docs citations

37
times ranked

2951
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Yersinia pestis</i> and the Plague of Justinian 541–543 AD: a genomic analysis. <i>Lancet Infectious Diseases</i> , 2014, 14, 319-326.	9.1	358
2	The large-scale blast score ratio (LS-BSR) pipeline: a method to rapidly compare genetic content between bacterial genomes. <i>PeerJ</i> , 2014, 2, e332.	2.0	265
3	NASP: an accurate, rapid method for the identification of SNPs in WGS datasets that supports flexible input and output formats. <i>Microbial Genomics</i> , 2016, 2, e000074.	2.0	237
4	17th Century Variola Virus Reveals the Recent History of Smallpox. <i>Current Biology</i> , 2016, 26, 3407-3412.	3.9	197
5	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. <i>Frontiers in Genetics</i> , 2015, 6, 235.	2.3	160
6	Defining the Phylogenomics of <i>Shigella</i> Species: a Pathway to Diagnostics. <i>Journal of Clinical Microbiology</i> , 2015, 53, 951-960.	3.9	82
7	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing <i>Clostridia</i> . <i>BMC Genomics</i> , 2016, 17, 180.	2.8	71
8	More than 50% of <i>Clostridium difficile</i> Isolates from Pet Dogs in Flagstaff, USA, Carry Toxigenic Genotypes. <i>PLoS ONE</i> , 2016, 11, e0164504.	2.5	64
9	A <i>Bacillus anthracis</i> Genome Sequence from the Sverdlovsk 1979 Autopsy Specimens. <i>MBio</i> , 2016, 7, .	4.1	52
10	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. <i>MBio</i> , 2016, 7, .	4.1	49
11	Unprecedented Melioidosis Cases in Northern Australia Caused by an Asian <i>Burkholderia pseudomallei</i> Strain Identified by Using Large-Scale Comparative Genomics. <i>Applied and Environmental Microbiology</i> , 2016, 82, 954-963.	3.1	46
12	<i>Burkholderia humptydoensis</i> sp. nov., a New Species Related to <i>Burkholderia thailandensis</i> and the Fifth Member of the <i>Burkholderia pseudomallei</i> Complex. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	45
13	Phylogenetically typing bacterial strains from partial SNP genotypes observed from direct sequencing of clinical specimen metagenomic data. <i>Genome Medicine</i> , 2015, 7, 52.	8.2	38
14	Population Structure and Genetic Diversity among Isolates of <i>Coccidioides posadasii</i> in Venezuela and Surrounding Regions. <i>MBio</i> , 2019, 10, .	4.1	28
15	<i>Burkholderia pseudomallei</i> , the causative agent of melioidosis, is rare but ecologically established and widely dispersed in the environment in Puerto Rico. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007727.	3.0	26
16	Genomic Characterization of <i>Burkholderia pseudomallei</i> Isolates Selected for Medical Countermeasures Testing: Comparative Genomics Associated with Differential Virulence. <i>PLoS ONE</i> , 2015, 10, e0121052.	2.5	25
17	Domestic canines do not display evidence of gut microbial dysbiosis in the presence of <i>Clostridioides (Clostridium) difficile</i> , despite cellular susceptibility to its toxins. <i>Anaerobe</i> , 2019, 58, 53-72.	2.1	20
18	Diverse <i>Burkholderia</i> Species Isolated from Soils in the Southern United States with No Evidence of <i>B. pseudomallei</i> . <i>PLoS ONE</i> , 2015, 10, e0143254.	2.5	20

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19	Reorganized Genomic Taxonomy of Francisellaceae Enables Design of Robust Environmental PCR Assays for Detection of <i>Francisella tularensis</i> . <i>Microorganisms</i> , 2021, 9, 146.	3.6	19
20	Differentiating <i>Botulinum</i> Neurotoxin-Producing <i>Clostridia</i> with a Simple, Multiplex PCR Assay. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	18
21	Pathogen to commensal? Longitudinal within-host population dynamics, evolution, and adaptation during a chronic >16-year <i>Burkholderia pseudomallei</i> infection. <i>PLoS Pathogens</i> , 2020, 16, e1008298.	4.7	12
22	Expanding the <i>Burkholderia pseudomallei</i> Complex with the Addition of Two Novel Species: <i>Burkholderia mayonis</i> sp. nov. and <i>Burkholderia savannae</i> sp. nov.. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0158321.	3.1	11
23	A chromosomal-level reference genome of the widely utilized <i>Coccidioides posadasii</i> laboratory strain "Silveira" G3: <i>Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	10
24	Selective whole genome amplification and sequencing of <i>Coxiella burnetii</i> directly from environmental samples. <i>Genomics</i> , 2020, 112, 1872-1878.	2.9	9
25	Whole-genome sequencing investigation of animal-skin-drum-associated UK anthrax cases reveals evidence of mixed populations and relatedness to a US case. <i>Microbial Genomics</i> , 2015, 1, e000039.	2.0	9
26	Genome Sequence of <i>Burkholderia pseudomallei</i> NCTC 13392. <i>Genome Announcements</i> , 2013, 1, .	0.8	8
27	Evolutionary history and current distribution of the West Mediterranean lineage of <i>Brucella melitensis</i> in Italy. <i>Microbial Genomics</i> , 2020, 6, .	2.0	8
28	<i>Burkholderia ubonensis</i> Meropenem Resistance: Insights into Distinct Properties of Class A β -Lactamases in <i>Burkholderia cepacia</i> Complex and <i>Burkholderia pseudomallei</i> Complex Bacteria. <i>MBio</i> , 2020, 11, .	4.1	7
29	A global to local genomics analysis of <i>Clostridioides difficile</i> ST1/RT027 identifies cryptic transmission events in a northern Arizona healthcare network. <i>Microbial Genomics</i> , 2019, 5, .	2.0	7
30	Conservation of Resistance-Nodulation-Cell Division Efflux Pump-Mediated Antibiotic Resistance in <i>Burkholderia cepacia</i> Complex and <i>Burkholderia pseudomallei</i> Complex Species. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, e0092021.	3.2	6
31	Draft Genome Sequence of the First Pathogenic <i>Leptospira</i> Isolates from Ecuador. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
32	Developing Inclusivity and Exclusivity Panels for Testing Diagnostic and Detection Tools Targeting <i>Burkholderia pseudomallei</i> , the Causative Agent of Melioidosis. <i>Journal of AOAC INTERNATIONAL</i> , 2018, 101, 1920-1926.	1.5	5
33	<i>Burkholderia ubonensis</i> High-Level Tetracycline Resistance Is Due to Efflux Pump Synergy Involving a Novel TetA(64) Resistance Determinant. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	3.2	5
34	<i>Burkholderia pseudomallei</i> in Soil, US Virgin Islands, 2019. <i>Emerging Infectious Diseases</i> , 2020, 26, 2773-2775.	4.3	4
35	Complete Genome Sequence of <i>Peptacetobacter</i> (<i>Clostridium</i>) <i>hiranonis</i> Strain DGF055142, Isolated from Dog Feces from Flagstaff, Arizona, USA, 2019. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	3
36	Multiple phylogenetically-diverse, differentially-virulent <i>Burkholderia pseudomallei</i> isolated from a single soil sample collected in Thailand. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010172.	3.0	3

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37	VNTR diversity in <i>Yersinia pestis</i> isolates from an animal challenge study reveals the potential for in vitro mutations during laboratory cultivation. <i>Infection, Genetics and Evolution</i> , 2016, 45, 297-302.	2.3	1